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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/470,735DATE: 06/13/96
TIME: 14:57:44

INPUT SET: SII056.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

#7

SEQUENCE LISTING

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Israeli, Ron S.
6 Heston, Warren D.W.
7 Fair, William R.
8
9 (ii) TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN
10
11 (iii) NUMBER OF SEQUENCES: 38
12
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: Cooper & Dunham LLP
15 (B) STREET: 1185 Avenue of the Americas
16 (C) CITY: New York
17 (D) STATE: New York
18 (E) COUNTRY: United States of America
19 (F) ZIP: 10036
20
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Floppy disk
23 (B) COMPUTER: IBM 330 466 DX2
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
26
27 (vi) CURRENT APPLICATION DATA:
28 (A) APPLICATION NUMBER: 08/470,735
29 (B) FILING DATE: 06-JUN-1995
30 (C) CLASSIFICATION:
31
32 (viii) ATTORNEY/AGENT INFORMATION:
33 (A) NAME: White, John P.
34 (B) REGISTRATION NUMBER: 28,678
35 (C) REFERENCE/DOCKET NUMBER: 1747/41426-D
36
37 (ix) TELECOMMUNICATION INFORMATION:
38 (A) TELEPHONE: (212) 278-0400
39 (B) TELEFAX: (212) 391-0525
40
41
42 (2) INFORMATION FOR SEQ ID NO:1:
43
44 (i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 2653 base pairs
46 (B) TYPE: nucleic acid

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47 (C) STRANDEDNESS: double
48 (D) TOPOLOGY: linear
49
50 (ii) MOLECULE TYPE: cDNA
51
52 (iii) HYPOTHETICAL: NO
53
54 (iv) ANTI-SENSE: NO
55
56 (vi) ORIGINAL SOURCE:
57 (A) ORGANISM: Homo sapiens
58 (F) TISSUE TYPE: Carcinoma
59
60 (vii) IMMEDIATE SOURCE:
61 (B) CLONE: Prostate-Specific Membrane Antigen
62
63 (ix) FEATURE:
64 (A) NAME/KEY: CDS
65 (B) LOCATION: 262..2511
66
67
68 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
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70 CTCAAAAGGG GCCGGATTTC CTTCTCCTGG AGGCAGATGT TGCCTCTCTC TCTCGCTCGG 60
71
72 ATTGGTTTCAG TGCACTCTAG AAACACTGCT GTGGTGGAGA AACTGGACCC CAGGTCTGGA 120
73
74 GCGAATTCCA GCCTGCAGGG CTGATAAGCG AGGCATTAGT GAGATTGAGA GAGACTTTAC 180
75
76 CCCGCCGTGG TGGTTGGAGG GCGCGCAGTA GAGCAGCAGC ACAGGGCGCGG GTCCCGGGAG 240
77
78 GCCGGCTCTG CTCGCGCCGA G ATG TGG AAT CTC CTT CAC GAA ACC GAC TCG 291
79 Met Trp Asn Leu Leu His Glu Thr Asp Ser
80 1 5 10
81
82 GCT GTG GCC ACC GCG CGC CGC CCG CGC TGG CTG TGC GCT GGG GCG CTG 339
83 Ala Val Ala Thr Ala Arg Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu
84 15 20 25
85
86 GTG CTG GCG GGT GGC TTC TTT CTC CTC GGC TTC CTC TTC GGG TGG TTT 387
87 Val Leu Ala Gly Gly Phe Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe
88 30 35 40
89
90 ATA AAA TCC TCC AAT GAA GCT ACT AAC ATT ACT CCA AAG CAT AAT ATG 435
91 Ile Lys Ser Ser Asn Glu Ala Thr Asn Ile Thr Pro Lys His Asn Met
92 45 50 55
93
94 AAA GCA TTT TTG GAT GAA TTG AAA GCT GAG AAC ATC AAG AAG TTC TTA 483
95 Lys Ala Phe Leu Asp Glu Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu
96 60 65 70
97
98 TAT AAT TTT ACA CAG ATA CCA CAT TTA GCA GGA ACA GAA CAA AAC TTT 531
99 Tyr Asn Phe Thr Gln Ile Pro His Leu Ala Gly Thr Glu Gln Asn Phe

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100	75	80	85	90	
101					
102	CAG CTT GCA AAG CAA ATT CAA TCC CAG TGG AAA GAA TTT GGC CTG GAT				579
103	Gln Leu Ala Lys Gln Ile Gln Ser Gln Trp Lys Glu Phe Gly Leu Asp				
104	95	100	105		
105					
106	TCT GTT GAG CTA GCA CAT TAT GAT GTC CTG TTG TCC TAC CCA AAT AAG				627
107	Ser Val Glu Leu Ala His Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys				
108	110	115	120		
109					
110	ACT CAT CCC AAC TAC ATC TCA ATA ATT AAT GAA GAT GGA AAT GAG ATT				675
111	Thr His Pro Asn Tyr Ile Ser Ile Ile Asn Glu Asp Gly Asn Glu Ile				
112	125	130	135		
113					
114	TTC AAC ACA TCA TTA TTT GAA CCA CCT CCT CCA GGA TAT GAA AAT GTT				723
115	Phe Asn Thr Ser Leu Phe Glu Pro Pro Pro Gly Tyr Glu Asn Val				
116	140	145	150		
117					
118	TCG GAT ATT GTA CCA CCT TTC AGT GCT TTC TCT CCT CAA GGA ATG CCA				771
119	Ser Asp Ile Val Pro Pro Phe Ser Ala Phe Ser Pro Gln Gly Met Pro				
120	155	160	165	170	
121					
122	GAG GGC GAT CTA GTG TAT GTT AAC TAT GCA CGA ACT GAA GAC TTC TTT				819
123	Glu Gly Asp Leu Val Tyr Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe				
124	175	180	185		
125					
126	AAA TTG GAA CGG GAC ATG AAA ATC AAT TGC TCT GGG AAA ATT GTA ATT				867
127	Lys Leu Glu Arg Asp Met Lys Ile Asn Cys Ser Gly Lys Ile Val Ile				
128	190	195	200		
129					
130	GCC AGA TAT GGG AAA GTT TTC AGA GGA AAT AAG GTT AAA AAT GCC CAG				915
131	Ala Arg Tyr Gly Lys Val Phe Arg Gly Asn Lys Val Lys Asn Ala Gln				
132	205	210	215		
133					
134	CTG GCA GGG GCC AAA GGA GTC ATT CTC TAC TCC GAC CCT GCT GAC TAC				963
135	Leu Ala Gly Ala Lys Gly Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr				
136	220	225	230		
137					
138	TTT GCT CCT GGG GTG AAG TCC TAT CCA GAT GGT TGG AAT CTT CCT GGA				1011
139	Phe Ala Pro Gly Val Lys Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly				
140	235	240	245	250	
141					
142	GGT GGT GTC CAG CGT GGA AAT ATC CTA AAT CTG AAT GGT GCA GGA GAC				1059
143	Gly Gly Val Gln Arg Gly Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp				
144	255	260	265		
145					
146	CCT CTC ACA CCA GGT TAC CCA GCA AAT GAA TAT GCT TAT AGG CGT GGA				1107
147	Pro Leu Thr Pro Gly Tyr Pro Ala Asn Glu Tyr Ala Tyr Arg Arg Gly				
148	270	275	280		
149					
150	ATT GCA GAG GCT GTT GGT CTT CCA AGT ATT CCT GTT CAT CCA ATT GGA				1155
151	Ile Ala Glu Ala Val Gly Leu Pro Ser Ile Pro Val His Pro Ile Gly				
152	285	290	295		

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153
 154 TAC TAT GAT GCA CAG AAG CTC CTA GAA AAA ATG GGT GGC TCA GCA CCA 1203
 155 Tyr Tyr Asp Ala Gln Lys Leu Leu Glu Lys Met Gly Gly Ser Ala Pro
 156 300 305 310
 157
 158 CCA GAT AGC AGC TGG AGA GGA AGT CTC AAA GTG CCC TAC AAT GTT GGA 1251
 159 Pro Asp Ser Ser Trp Arg Gly Ser Leu Lys Val Pro Tyr Asn Val Gly
 160 315 320 325 330
 161
 162 CCT GGC TTT ACT GGA AAC TTT TCT ACA CAA AAA GTC AAG ATG CAC ATC 1299
 163 Pro Gly Phe Thr Gly Asn Phe Ser Thr Gln Lys Val Lys Met His Ile
 164 335 340 345
 165
 166 CAC TCT ACC AAT GAA GTG ACA AGA ATT TAC AAT GTG ATA GGT ACT CTC 1347
 167 His Ser Thr Asn Glu Val Thr Arg Ile Tyr Asn Val Ile Gly Thr Leu
 168 350 355 360
 169
 170 AGA GGA GCA GTG GAA CCA GAC AGA TAT GTC ATT CTG GGA GGT CAC CGG 1395
 171 Arg Gly Ala Val Glu Pro Asp Arg Tyr Val Ile Leu Gly Gly His Arg
 172 365 370 375
 173
 174 GAC TCA TGG GTG TTT GGT ATT GAC CCT CAG AGT GGA GCA GCT GTT 1443
 175 Asp Ser Trp Val Phe Gly Gly Ile Asp Pro Gln Ser Gly Ala Ala Val
 176 380 385 390
 177
 178 GTT CAT GAA ATT GTG AGG AGC TTT GGA ACA CTG AAA AAG GAA GGG TGG 1491
 179 Val His Glu Ile Val Arg Ser Phe Gly Thr Leu Lys Lys Glu Gly Trp
 180 395 400 405 410
 181
 182 AGA CCT AGA AGA ACA ATT TTG TTT GCA AGC TGG GAT GCA GAA GAA TTT 1539
 183 Arg Pro Arg Arg Thr Ile Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe
 184 415 420 425
 185
 186 GGT CTT CTT GGT TCT ACT GAG TGG GCA GAG GAG AAT TCA AGA CTC CTT 1587
 187 Gly Leu Leu Gly Ser Thr Glu Trp Ala Glu Glu Asn Ser Arg Leu Leu
 188 430 435 440
 189
 190 CAA GAG CGT GGC GTG GCT TAT ATT AAT GCT GAC TCA TCT ATA GAA GGA 1635
 191 Gln Glu Arg Gly Val Ala Tyr Ile Asn Ala Asp Ser Ser Ile Glu Gly
 192 445 450 455
 193
 194 AAC TAC ACT CTG AGA GTT GAT TGT ACA CCG CTG ATG TAC AGC TTG GTA 1683
 195 Asn Tyr Thr Leu Arg Val Asp Cys Thr Pro Leu Met Tyr Ser Leu Val
 196 460 465 470
 197
 198 CAC AAC CTA ACA AAA GAG CTG AAA AGC CCT GAT GAA GGC TTT GAA GGC 1731
 199 His Asn Leu Thr Lys Glu Leu Lys Ser Pro Asp Glu Gly Phe Glu Gly
 200 475 480 485 490
 201
 202 AAA TCT CTT TAT GAA AGT TGG ACT AAA AAA AGT CCT TCC CCA GAG TTC 1779
 203 Lys Ser Leu Tyr Glu Ser Trp Thr Lys Lys Ser Pro Ser Pro Glu Phe
 204 495 500 505
 205

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206	AGT GGC ATG CCC AGG ATA AGC AAA TTG GGA TCT GGA AAT GAT TTT GAG	1827
207	Ser Gly Met Pro Arg Ile Ser Lys Leu Gly Ser Gly Asn Asp Phe Glu	
208	510	515
209		520
210	GTG TTC TTC CAA CGA CTT GGA ATT GCT TCA GGC AGA GCA CGG TAT ACT	1875
211	Val Phe Phe Gln Arg Leu Gly Ile Ala Ser Gly Arg Ala Arg Tyr Thr	
212	525	530
213		535
214	AAA AAT TGG GAA ACA AAC AAA TTC AGC GGC TAT CCA CTG TAT CAC AGT	1923
215	Lys Asn Trp Glu Thr Asn Lys Phe Ser Gly Tyr Pro Leu Tyr His Ser	
216	540	545
217		550
218	GTC TAT GAA ACA TAT GAG TTG GTG GAA AAG TTT TAT GAT CCA ATG TTT	1971
219	Val Tyr Glu Thr Tyr Glu Leu Val Glu Lys Phe Tyr Asp Pro Met Phe	
220	555	560
221		565
222	570	
223	AAA TAT CAC CTC ACT GTG GCC CAG GTT CGA GGA GGG ATG GTG TTT GAG	2019
224	Lys Tyr His Leu Thr Val Ala Gln Val Arg Gly Gly Met Val Phe Glu	
225	575	580
226		585
227	CTA GCC AAT TCC ATA GTG CTC CCT TTT GAT TGT CGA GAT TAT GCT GTA	2067
228	Leu Ala Asn Ser Ile Val Leu Pro Phe Asp Cys Arg Asp Tyr Ala Val	
229	590	595
230		600
231	2115	
232	GTT TTA AGA AAG TAT GCT GAC AAA ATC TAC AGT ATT TCT ATG AAA CAT	
233	Val Leu Arg Lys Tyr Ala Asp Lys Ile Tyr Ser Ile Ser Met Lys His	
234	605	610
235		615
236	2163	
237	CCA CAG GAA ATG AAG ACA TAC AGT GTA TCA TTT GAT TCA CTT TTT TCT	
238	Pro Gln Glu Met Lys Thr Tyr Ser Val Ser Phe Asp Ser Leu Phe Ser	
239	620	625
240		630
241	2211	
242	GCA GTA AAG AAT TTT ACA GAA ATT GCT TCC AAG TTC AGT GAG AGA CTC	
243	Ala Val Lys Asn Phe Thr Glu Ile Ala Ser Lys Phe Ser Glu Arg Leu	
244	635	640
245		645
246		650
247	2259	
248	CAG GAC TTT GAC AAA AGC AAC CCA ATA GTA TTA AGA ATG ATG AAT GAT	
249	Gln Asp Phe Asp Lys Ser Asn Pro Ile Val Leu Arg Met Met Asn Asp	
250	655	660
251		665
252	2307	
253	CAA CTC ATG TTT CTG GAA AGA GCA TTT ATT GAT CCA TTA GGG TTA CCA	
254	Gln Leu Met Phe Leu Glu Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro	
255	670	675
256		680
257	2355	
258	GAC AGG CCT TTT TAT AGG CAT GTC ATC TAT GCT CCA AGC AGC CAC AAC	
259	Asp Arg Pro Phe Tyr Arg His Val Ile Tyr Ala Pro Ser Ser His Asn	
260	685	690
261		695
262	2403	
263	AAG TAT GCA GGG GAG TCA TTC CCA GGA ATT TAT GAT GCT CTG TTT GAT	
264	Lys Tyr Ala Gly Glu Ser Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp	
265	700	705
266		710
267	2451	
268	ATT GAA AGC AAA GTG GAC CCT TCC AAG GCC TGG GGA GAA GTG AAG AGA	